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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=1; day=18; hr=17; min=20; sec=53; ms=127; ]

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\*\*\*\*\*

Reviewer Comments:

<210> SEQ ID NO 1

<211> LENGTH: 35

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

Please remove all line headers from the sequence listing, i.e. SEQ ID  
NO, LENGTH:, TYPE: ...etc.

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Application No: 10500240

Version No: 2.0

**Input Set:****Output Set:****Started:** 2007-12-28 12:28:19.445**Finished:** 2007-12-28 12:28:24.889**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 444 ms**Total Warnings:** 23**Total Errors:** 31**No. of SeqIDs Defined:** 106**Actual SeqID Count:** 106

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
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W 213	Artificial or Unknown found in <213> in SEQ ID (5)
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W 213	Artificial or Unknown found in <213> in SEQ ID (7)
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W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

**Input Set:**

**Output Set:**

**Started:** 2007-12-28 12:28:19.445  
**Finished:** 2007-12-28 12:28:24.889  
**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 444 ms  
**Total Warnings:** 23  
**Total Errors:** 31  
**No. of SeqIDs Defined:** 106  
**Actual SeqID Count:** 106

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (24)
E 257	Invalid sequence data feature in <221> in SEQ ID (24)
E 257	Invalid sequence data feature in <221> in SEQ ID (26)
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E 257	Invalid sequence data feature in <221> in SEQ ID (38)
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E 257	Invalid sequence data feature in <221> in SEQ ID (68)
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E 257	Invalid sequence data feature in <221> in SEQ ID (78)
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<110> APPLICANT: GLYCOFI, INC.  
 <120> TITLE OF INVENTION: METHODS TO ENGINEER MAMMALIAN-TYPE CARBOHYDRATE  
 STRUCTURES  
 <130> FILE REFERENCE: GFI/102 PCT  
  
 <140> CURRENT APPLICATION NUMBER:10500240  
 <141> CURRENT FILING DATE:2005-03-23  
 <150> PRIOR APPLICATION NUMBER: 60/344,169  
 <151> PRIOR FILING DATE: 2001-12-27  
 <160> NUMBER OF SEQ ID NOS: 106  
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 <212> TYPE: DNA  
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 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
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<210> SEQ ID NO 17  
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 <220> FEATURE:  
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 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 18  
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 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
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<210> SEQ ID NO 21  
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 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
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<210> SEQ ID NO 22  
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 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 <400> SEQUENCE: 22  
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<210> SEQ ID NO 23  
 <211> LENGTH: 4  
 <212> TYPE: PRT  
 <213> ORGANISM: Saccharomyces cerevisiae  
 <400> SEQUENCE: 23  
 His Asp Glu Leu  
 1

<210> SEQ ID NO 24  
 <211> LENGTH: 458  
 <212> TYPE: PRT  
 <213> ORGANISM: Saccharomyces cerevisiae  
 <220> FEATURE:  
 <221> NAME/KEY: MOD\_RES  
 <222> LOCATION: (304)..(318)  
 <223> OTHER INFORMATION: Variable amino acid  
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 <221> NAME/KEY: MOD\_RES



<222> LOCATION: (416)..(436)

<223> OTHER INFORMATION: Variable amino acid

<400> SEQUENCE: 24

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Gln	Phe	Val	Arg	Pro	Pro	Leu	Asp	Leu	Trp	Gln	Asp	Leu	Lys	Asp	Gly
			20					25					30		
Val	Arg	Tyr	Val	Ile	Phe	Asp	Cys	Arg	Ala	Asn	Leu	Ile	Val	Met	Pro
			35				40					45			
Leu	Leu	Ile	Leu	Phe	Glu	Ser	Met	Leu	Cys	Lys	Ile	Ile	Ile	Lys	Lys
			50				55					60			
Val	Ala	Tyr	Thr	Glu	Ile	Asp	Tyr	Lys	Ala	Tyr	Met	Glu	Gln	Ile	Glu
					70					75					80
Met	Ile	Gln	Leu	Asp	Gly	Met	Leu	Asp	Tyr	Ser	Gln	Val	Ser	Gly	Gly
				85					90					95	
Thr	Gly	Pro	Leu	Val	Tyr	Pro	Ala	Gly	His	Val	Leu	Ile	Tyr	Lys	Met
			100					105						110	
Met	Tyr	Trp	Leu	Thr	Glu	Gly	Met	Asp	His	Val	Glu	Arg	Gly	Gln	Val
			115				120					125			
Phe	Phe	Arg	Tyr	Leu	Tyr	Leu	Leu	Thr	Leu	Ala	Leu	Gln	Met	Ala	Cys
			130			135					140				
Tyr	Tyr	Leu	Leu	His	Leu	Pro	Pro	Trp	Cys	Val	Val	Leu	Ala	Cys	Leu
145					150					155					160
Ser	Lys	Arg	Leu	His	Ser	Ile	Tyr	Val	Leu	Arg	Leu	Phe	Asn	Asp	Cys
				165				170					175		
Phe	Thr	Thr	Leu	Phe	Met	Val	Val	Thr	Val	Leu	Gly	Ala	Ile	Val	Ala
			180					185					190		
Ser	Arg	Cys	His	Gln	Arg	Pro	Lys	Leu	Lys	Lys	Ser	Leu	Ala	Leu	Val
			195				200					205			
Ile	Ser	Ala	Thr	Tyr	Ser	Met	Ala	Val	Ser	Ile	Lys	Met	Asn	Ala	Leu
			210			215					220				
Leu	Tyr	Phe	Pro	Ala	Met	Met	Ile	Ser	Leu	Phe	Ile	Leu	Asn	Asp	Ala
225					230					235				240	
Asn	Val	Ile	Leu	Thr	Leu	Leu	Asp	Leu	Val	Ala	Met	Ile	Ala	Trp	Gln
				245					250					255	
Val	Ala	Val	Ala	Val	Pro	Phe	Leu	Arg	Ser	Phe	Pro	Gln	Gln	Tyr	Leu
			260					265					270		
His	Cys	Ala	Phe	Asn	Phe	Gly	Arg	Lys	Phe	Met	Tyr	Gln	Trp	Ser	Ile
			275				280					285			
Asn	Trp	Gln	Met	Met	Asp	Glu	Ala	Phe	Asn	Asp	Lys	Arg	Phe	Xaa	
			290			295				300					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Val
305					310					315				320	
Thr	Arg	Tyr	Pro	Arg	Ile	Leu	Pro	Asp	Leu	Trp	Ser	Ser	Leu	Cys	His
				325					330					335	
Pro	Leu	Arg	Lys	Asn	Ala	Val	Leu	Asn	Ala	Asn	Pro	Ala	Lys	Thr	Ile
			340					345					350		
Pro	Phe	Val	Leu	Ile	Ala	Ser	Asn	Phe	Ile	Gly	Val	Leu	Phe	Ser	Arg
			355				360					365			
Ser	Leu	His	Tyr	Gln	Phe	Leu	Ser	Trp	Tyr	His	Trp	Thr	Leu	Pro	Ile
			370			375					380				
Leu	Ile	Phe	Trp	Ser	Gly	Met	Pro	Phe	Phe	Val	Gly	Pro	Ile	Trp	Tyr
385					390					395				400	
Val	Leu	His	Glu	Trp	Cys	Trp	Asn	Ser	Tyr	Pro	Pro	Asn	Ser	Gln	Xaa
				405					410					415	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			420				425					430			

Xaa Xaa Xaa Xaa Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg  
           435                          440                          445  
 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn  
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<210> SEQ ID NO 25

<211> LENGTH: 458

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 25

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 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly  
                           20                          25                          30  
 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro  
                           35                          40                          45  
 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys  
                           50                          55                          60  
 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu  
   65                          70                          75                          80  
 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly  
                           85                          90                          95  
 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met  
                           100                          105                          110  
 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val  
                           115                          120                          125  
 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys  
   130                          135                          140  
 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu  
   145                          150                          155                          160  
 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys  
                           165                          170                          175  
 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala  
                           180                          185                          190  
 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val  
                           195                          200                          205  
 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu  
   210                          215                          220  
 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala  
   225                          230                          235                          240  
 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln  
                           245                          250                          255  
 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu  
                           260                          265                          270  
 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile  
                           275                          280                          285  
 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His  
   290                          295                          300  
 Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val  
   305                          310                          315                          320  
 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His  
                           325                          330                          335  
 Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile  
                           340                          345                          350  
 Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg  
                           355                          360                          365  
 Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile

370	375	380
Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr		
385	390	395
Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala		400
	405	410
Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala		415
	420	425
Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg		430
	435	440
Thr Thr Ser Ser Met Glu Lys Lys Leu Asn		445
450	455	

<210> SEQ ID NO 26

<211> LENGTH: 443

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<220> FEATURE:

<221> NAME/KEY: MOD\_RES

<222> LOCATION: (333)..(347)

<223> OTHER INFORMATION: Variable amino acid

<400> SEQUENCE: 26

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Ala	Asn	Leu	Ile	Val	Met	Pro	Leu	Leu	Ile	Leu	Phe	Glu	Ser	Met	Leu
		20					25					30			
Cys	Lys	Ile	Ile	Ile	Lys	Lys	Val	Ala	Tyr	Thr	Glu	Ile	Asp	Tyr	Lys
	35					40					45				
Ala	Tyr	Met	Glu	Gln	Ile	Glu	Met	Ile	Gln	Leu	Asp	Gly	Met	Leu	Asp
	50					55				60					
Tyr	Ser	Gln	Val	Ser	Gly	Gly	Thr	Gly	Pro	Leu	Val	Tyr	Pro	Ala	Gly
	65				70				75					80	
His	Val	Leu	Ile	Tyr	Lys	Met	Met	Tyr	Trp	Leu	Thr	Glu	Gly	Met	Asp
			85					90						95	
His	Val	Glu	Arg	Gly	Gln	Val	Phe	Phe	Arg	Tyr	Leu	Tyr	Leu	Leu	Thr
		100					105						110		
Leu	Ala	Leu	Gln	Met	Ala	Cys	Tyr	Tyr	Leu	Leu	His	Leu	Pro	Pro	Trp
	115					120					125				
Cys	Val	Val	Leu	Ala	Cys	Leu	Ser	Lys	Arg	Leu	His	Ser	Ile	Tyr	Val
	130					135				140					
Leu	Arg	Leu	Phe	Asn	Asp	Cys	Phe	Thr	Thr	Leu	Phe	Met	Val	Val	Thr
	145			150					155					160	
Val	Leu	Gly	Ala	Ile	Val	Ala	Ser	Arg	Cys	His	Gln	Arg	Pro	Lys	Leu
		165					170					175			
Lys	Lys	His	Gln	Thr	Cys	Lys	Val	Pro	Pro	Phe	Val	Phe	Phe	Phe	Met
		180					185					190			
Cys	Cys	Ala	Ser	Tyr	Arg	Val	His	Ser	Ile	Phe	Val	Leu	Arg	Leu	Phe
	195					200					205				
Asn	Asp	Pro	Val	Ala	Met	Val	Leu	Leu	Phe	Leu	Ser	Ile	Asn	Leu	Leu
	210				215					220					
Leu	Ala	Gln	Arg	Trp	Gly	Trp	Gly	Ser	Leu	Ala	Leu	Val	Ile	Ser	Ala
	225			230					235					240	
Thr	Tyr	Ser	Met	Ala	Val	Ser	Ile	Lys	Met	Asn	Ala	Leu	Leu	Tyr	Phe
		245					250							255	
Pro	Ala	Met	Met	Ile	Ser	Leu	Phe	Ile	Leu	Asn	Asp	Ala	Asn	Val	Ile
	260						265					270			
Leu	Thr	Leu	Leu	Asp	Leu	Val	Ala	Met	Ile	Ala	Trp	Gln	Val	Ala	Val
	275					280					285				

Ala	Val	Pro	Phe	Leu	Arg	Ser	Phe	Pro	Gln	Gln	Tyr	Leu	His	Cys	Ala
290						295					300				
Phe	Asn	Phe	Gly	Arg	Lys	Phe	Met	Tyr	Gln	Trp	Ser	Ile	Asn	Trp	Gln
305					310					315					320
Met	Met	Asp	Glu	Glu	Ala	Phe	Asn	Asp	Lys	Arg	Phe	Xaa	Xaa	Xaa	Xaa
			325						330					335	